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us-09-758-493-1_copy_1_188.rag

Tue Nov 15 15:32:23 2005

Page 1

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OM protein - protein search, using sw model

Run on: November 14, 2005, 17:04:13 ; Search time 163 Seconds

(without alignment) 446,079 Million cell updates/sec

Title: US-09-758-493-1_COPY 1_188

Perfect score: 965

Sequence: 1 CPOEDSIAPINGSSSTIP... YPQNNFEALKTQNQRK 188

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 2105692 seqs, 186760381 residues

Total number of hits satisfying chosen parameters: 1413077

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Maximum Match 0*

Listing first 45 summaries

Database : A_Geneseq_16Dec04:

- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003s:*
 - 7: geneseqp2003s:*
 - 8: geneseqp2004s:*
- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	960	99.5	187	2	AAY21991		AY21991; Human com
2	893	92.5	177	5	AAT76866		Aau76866; Human int
3	890	92.5	177	5	AAT76855		Aau76855; Human int
4	534	55.3	187	2	AAY21992		Aay21992; Human com
5	323	55.3	176	5	ABB78816		Abb78816; Von Wille
6	286	55	184	3	AAY2339		Aay2339; Human CD1
7	286	55	184	6	ADG3895		Adg3895; Human EXP
8	286	55	184	8	ADR03370		Adr03370; Human CD1
10	286	55	187	8	ADR23224		Adr23224; Human int
11	282	55	180	5	ABY76376		Abby76376; Lymphocyte
12	281	55	180	3	AAY2330		Aay2330; Rhesus CD
13	281	55	184	8	ADG38956		Adg38956; Monkey CD
14	281	55	184	8	ADR03371		Adr03371; Rhesus ma
15	276	55	184	8	AAT76848		Aau76848; Human int
16	276	55	184	5	AAT76849		Aau76849; Human int
17	262	55	181	4	ABU22684		Abu22684; Cell strn
18	231	55	178	3	AAB08817		Aab08817; A von Wille
19	192	55	180	5	ABP4907		Abp4907; Von Wille
20	171	55	177	33	AAR0292		Aar0292; Beta-2 in
21	171	55	177	33	AAW0204		Aaw0204; Human bet
22	171	55	116	7	ABM05598		Abm05598; Mouse pro
23	162	55	168	6	AAE32503		Aae32503; Mouse von
24	160	55	168	6	AAE32500		Aae32500; Human von
25	155	55	160	3	AAE08816		Aae08816; A von Wille

RESULT 1
AY21991
ID AAY21991 standard; protein; 187 AA.

XX
AC AAY21991;
XX
DR 13-SEP-1999 (first entry)
XX
DS Human complement factor MAC-1 vWF domain sequence.
XX
XX Factor B analogue; modified; complement activity; complement factor B;
KW short consensus repeat domain; von Willebrand Factor domain; human; C;
KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
KW myocardial infarction; acute shock lung syndrome; inflammation; vWF;
XX
OS Homo sapiens.
XX
PN USS928892-A.
XX
XX
PD 27-JUL-1999.
XX
PP 26-JUL-1996; 96US-00687706.
XX
PR 03-JAN-1994; 94US-00177109.
XX
PA (UNIV) UNIV WASHINGTON.
XX
PI Oglesby TJ, Hourcade DS,
XX
DR WPI; 1999-429498/36.
XX
PT Nucleic acids encoding complement protein homologues useful for
modulating function of the complement system in the treatment of a
variety of immune and autoimmune complex mediated syndromes.
XX
BS Disclosure; Fig 5a-B; 53pp; English.
XX
CC The invention relates to a Factor B analogue that exhibits modified
complement activity in vitro. The analogue is generated by substituting a
short consensus repeat domain (SCR) or a von Willebrand Factor domain
(vWF) of human factor B with a SCR or a vWF from a second protein such as
human C2 or CR1. The analogues may be used to regulate the complement
system involved in immune and autoimmune responses. Complement activity
can account for substantial tissue damage in a wide variety of autoimmune
immune complex mediated syndromes such as lupus erythematosus,
rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
of the complement system using the analogues is likely to provide a means

CC of therapeutic intervention in these cases. Inhibition of complement may
 CC also be favorable in cases that involve tissue damage caused by vascular
 CC injury such as myocardial infarction, cerebral vascular accidents or
 CC acute shock lung syndrome. In these cases the complement system may
 CC contribute to the destruction of partially damaged tissue as in
 CC the case of inflammation. Complement inhibition is important in
 CC the prevention of xeno-gene rejection (the inhibition of complement by
 CC cell associated and soluble inhibitors is useful in protecting the
 CC transplant from damage caused by activation of endogenous complement. The
 CC present sequence represents the vWF domain of human factor Mac-1
 XX

SQ Sequence 187 AA:

```

Query Match 99.5%; Score 950; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 1. 4e-97;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPQDSPIALDGS5LIPDFRDKMPEVSTMEQLKSTLPSLMQYSEPRHPTPK 60
  1 CPQDSPIALDGS5LIPDFRDKMPEVSTMEQLKSTLPSLMQYSEPRHPTPK 60
  DB 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  Qy 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  DB 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  Qy 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFBALKT 180
  DB 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFEALKT 180
  Qy 181 1QNLRE 187
  DB 181 1QNLRE 187
```

RESULT 2

AAU76866 standard; protein; 177 AA.

AAU76866;

DT 21-MAY-2002 (first entry)

DB Human integrin alpha subunit CD1b deletion variant A domain #2.

XX Human; integrin alpha subunit; A domain; CD1b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; reconstitutive;
 KW ischaemic reperfusion injury; immune complex; parasitic disease; mutant;
 KW antinflammatory; vasoconstrictor; antiparasitic; viliary; gene therapy;
 KW mutant.

OS Homo sapiens.

XX Synthetic.

EH Location/Qualifiers

PT Misc-difference 172 /note= "Wild-type Val substituted by Cys"

PT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"

PN WO200209737-A1.

XX 07-FEB-2002.

PD 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-022909P.

PR 11-JAN-2001; 2001US-007893.

PR 13-MAR-2001; 2001US-0080534.

XX (GBHO) GEN HOSPITAL CORP.

XX

P1 Arnautov AM, Li R, Xiong J;
 XX WPI: 2002-188667-4.

DR Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases. Comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX

PS Claim 21: Page: 55pp; English.

XX The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC integrin beta subunit A domain where I, an residue 312 has been replaced by
 CC G or A, at residue 313 and A at residue 314 have been replaced by C or
 CC V at residue 315 and A at residue 316 have been replaced by C is useful
 CC for determining if a compound is a candidate compound for binding to
 CC collagen or treating an inflammatory disorder. By contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complex, parasitic diseases,
 CC purify variant integrin polypeptides, reagents and as tools for probing in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD1b deletion variant A domain. Note: This
 CC variant sequence is not featured in the specification but has been
 CC derived from the wild-type protein shown in AAU76847.

SO Sequence 177 AA:

```

Query Match 92.5%; Score 893; DB 5; Length 177;
Best Local Similarity 97.7%; Pred. No. 3. 4e-90;
Matches 172; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPQDSPIALDGS5LIPDFRDKMPEVSTMEQLKSTLPSLMQYSEPRHPTPK 60
  1 CPQDSPIALDGS5LIPDFRDKMPEVSTMEQLKSTLPSLMQYSEPRHPTPK 60
  DB 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  Qy 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  DB 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  Qy 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFE 176
  DB 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFE 176
  Qy 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  DB 61 BFOQNPNPISLVKEPTOLGLRTHTGKRVBLNTGARNAKFLVLTGDKFG 120
  Qy 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFE 176
  DB 121 DPGYESVTPADERGTVRYIGVDAFREKSRQELNITASKSPRDYFQNNFE 176
```

RESULT 3

AAU76865 standard; protein; 177 AA.

AAU76865;

AC AC

XX 21-MAY-2002 (first entry)

DB Human integrin alpha subunit CD1b deletion variant A domain #1.

XX Human; integrin alpha subunit; A domain; CD1b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; reconstitutive;
 KW ischaemic reperfusion injury; immune complex; parasitic disease; mutant;
 KW antinflammatory; vasoconstrictor; antiparasitic; viliary; gene therapy;
 KW mutant.

OS Homo sapiens.

XX Synthetic.

EH Location/Qualifiers

PT Key

PT Misc-difference 172 /note= "Wild-type Phe substituted by Cys"

PT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"

PN WO200209737-A1.

XX 07-FEB-2002.

PD 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-022909P.

PR 11-JAN-2001; 2001US-007893.

PR 13-MAR-2001; 2001US-0080534.

XX (GBHO) GEN HOSPITAL CORP.

XX

Key

PT Misc-difference 170 /note= "Wild-type Phe substituted by Cys"

PT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"

PN WO200209737-A1.

CR3 - autoimmune response; tissue damage; lupus erythematosus; therapy;
 rheumatoïd arthritis; hemolytic anemia; myasthenia gravis; injury;
 myocardial infarction; acute shock lung syndrome; inflammation; vWF.

AC ABB78816;
 XX
 DT 29-JUL-2002 (First entry)
 DS Von Willebrand factor type A domain protein SEQ ID NO:18.
 KW Human; NOX; cytosolic; antiatherosclerotic; cardiovascular; lymphoma;
 KW antiidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
 KW cardiomyopathy; atherosclerotic; cell signal processing; diabetes; AIDS;
 KW metabolic pathway modulation; neoplastic; neurological disorder; asthma;
 KW adenocarcinoma; prostate cancer; uterus cancer; immune response;
 KW Crohn's disease; multiple sclerosis; Graft versus host disease.
 XX Unidentified.
 XX
 PN WO2002010974-A2.
 PD 18-APR-2002.
 PP 12-OCT-2001; 2001WO-US031922.
 XX
 PR 12-OCT-2000; 2000US-020113P.
 PR 16-OCT-2000; 2000US-0200635P.
 PR 16-OCT-2000; 2000US-0200637P.
 PR 16-OCT-2000; 2000US-0200648P.
 PR 16-OCT-2000; 2000US-0200649P.
 PR 16-OCT-2000; 2000US-0200652P.
 PR 16-OCT-2000; 2000US-0200659P.
 PR 16-OCT-2000; 2000US-0200703P.
 PR 16-OCT-2000; 2000US-0200722P.
 PR 16-OCT-2000; 2000US-021190P.
 PR 18-JAN-2001; 2001US-022455P.
 XX
 (CUDRA-) CURAGEN CORP.
 (MILL.) MILLER I.
 PI Grossé WM, Alsobrook JP, Lepley DM, Burgess CB, Mishra V, Shimamoto RA, Szczerba BD, Spyrek KA;
 PI Li L, Padias RA, Edinger S, Gerlach V, Nadgoudali J, Stone D, Gunther E, Silberman K;
 DR WPI: 2002-4411247.
 PT New NOX polypeptides and polynucleotides, useful for treating or preventing a NOX-associated pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes.
 XX
 Disclosure: Page 62; 227pp; English.
 XX
 The present invention describes novel human proteins designated NOX (where X is 1, 2a, 2b, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOVA-d are keratin 4-like proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like protein; NOV5 is a serotonin receptor-like protein; NOV6 and NOV65 are cold inducible glycoprotein 30-like proteins; NOV7 is a matrin-2-like protein; NOV8 is a leucocyte surface antigen (CD53)-like protein; and NOV9 is a tyrosine kinase-like protein. NOX sequences have cytotoxic, antiangiogenic, cardiovascular, antidiabetic, immunosuppressive and neuroprotective activities, and can be used in gene therapy. The NOX sequences can be used in diagnostics, particularly for treating, preventing or alleviating a NOX-associated disorder, or a pathological state in a subject, particularly a human. These disorders include cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOX polypeptide or nucleic acid, particularly cancer. The NOX sequences are especially useful in therapeutic or prophylactic applications for neoplastic or neurological disorders, and in the treatment of adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence represents a von Willebrand factor type A domain protein sequence which is given in a domain analysis comparison with the human NOV7 protein from the present invention.

XX Sequence 176 AA;
 SQ Query Match 34.6%; Score 333.5; DB 5; Length 176;
 Best Local Similarity 43.4%; Pre No. 2.8e-285; Indels 9; Gaps 4;
 Matches 79; Conservative 29; Wimatches 65; Indel 9; Gaps 4;
 Oy 7 DIAPLODOSSTIPDOPRMKEFYSTUMFOLK- KSKTLESLMYSSEFRHTFEKFEN 64
 Db 1 DIVFLDOSSTGQFNFEDTPVERFLDGPDRYGLVQSDWAVREPKLADQN 60
 Qy 65 NNPNSLAKPATOL-LGRHTATCIRKORELFTNTGANKAOKAQLILUVITDSEKFGDPD 123
 Db 61 KQBVQALKRQIYQAGGNGTALQIVRNFTTEASGREGAPVVLIDERSQDPD 120
 Qy 124 GVEDVTPARDEGVRYTGVDGFPSERGSRBLNTASKPRDYNPQNPMLALITION 183
 Db 121 -- RDVNLNKKAGVNPALGQNADNVB--- EUREIAKPDQEHRVFSDFBALDTQ 174
 Qy 184 QL 195
 Db 175 LL 176

RESULT 6
 AA Y82249
 ID AA82249 standard; protein; 184 AA.
 XX
 AC AA82249;
 DE Humanised; anti-CD1a; antibody; anti-inflammatory; immunosuppressant;
 KW tumour; antibody; anti-inflammatory; immunological response; IgA1;
 KW lymphocyte function associated antigen; IgE; IgG1; IgG3; IgM; IgG; IgA; IgD;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 Homo sapiens.
 OS XX
 PN US6037454-A.
 PD 22-JUN-2000 (First entry)
 XX
 DE Human CD1a I-domain amino acid sequence SEQ ID NO:7.
 XX
 KW Humanised; anti-CD1a; antibody; anti-inflammatory; immunosuppressant;
 KW tumour; antibody; anti-inflammatory; immunological response; IgA1;
 KW lymphocyte function associated antigen; IgE; IgG1; IgG3; IgM; IgG; IgD;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 Homo sapiens.
 OS XX
 PN US6037454-A.
 PD 14-MAR-2000.
 XX
 PS 20-NOV-1997; 97US-00974899.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 XX
 (GSTH) GENENTECH INC.
 PR Jardini PM, Presta LG;
 PR WPI; 2000-282241/24.
 XX
 PR New humanized anti-CD1a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable region complementarity determining regions.
 PR
 PS Example: Fig 2; 38pp; English.
 XX
 CC The present invention describes a humanised anti-CD1a antibody (Ab) that binds specifically to the human CD1a I-domain. The Ab has anti-inflammatory, immunosuppressive, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (IgA1) which is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab is used (i) optionally when coupled to a cytokinin, to treat or prevent disorders defined by lymphocyte function-associated antigen-1 (IgA1; CD1a/CD1b), e.g. sarcoidosis, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukaemia, viral infections, also for inhibiting graft rejection; (ii) when labelled, to detect CD1a; (iii) for

PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1995; 99US-00420745.
 (GUTH) GENENTECH INC.
 PA XX
 Jardieu PM, Prete LG;
 WPI: 2004-05151/05.

XX Humanized anti-CD1a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 PS Example: SEQ ID NO 7; 43pp; English.

CC The invention relates to a Humanised anti-cluster of differentiation (CD)1a antibody having specificity to human CD1a I-domain or CD1a with a kd value of not more than 1x10⁻⁸ M, or concentration for 50% inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte epidermal keratinocytes expressing adhesion molecule (ICAM 1).
 CC Also included are a kit comprising the antibody and instructions for use to detect the CD1a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody binds to epitope MH24 on CD1a. The antibody is useful for determining the presence of CD1a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a activating enzyme, or as an affinity purification agent. The present sequence is the Human CD1a I-domain, the target for the antibody of the invention.
 CC Sequence 164 AA;

Query Match 29 7%; Score 286.5; DB 8; Length 164;
 Best Local Similarity 33.5%; Prcd No. 4.7e-21;
 Matches 61; Conservative 47; Missmatches 67; Indels 7; Gaps 2;

Qy 7 DPAFDGSSSIIPDPFRKKEFVSTYMEQLKSKTFLSMOYSEBRPRTMPPEKFQNNP 66
 Db 5 DPAFDGSSSIIPDPFRKKEFVSTYMEQLKSKTFLSMOYSEBRPRTMPPEKFQNNP 64
 Qy 67 NPSLIVKPTDOLGHHTATGIRKVRBFNTINGARQPKILWVTDSEKGCPDLYE 126
 Db 65 DDALLKXHMLLNTPGANTVATPFRBLGARDPATVLLIDDE--ATDSGNI 122
 Qy 127 DYPDADEREGVITYRIGYDGFASRSKSRQBLNTASPRDPRFVQVNRLAQTQNL 186
 Db 123 DAQD----IIRRIGKICKPQTKEQSTQULKAPSKAPBVKLDFKLDLFTEQ 177
 Qy 187 EK 188
 Db 178 KX 179

RESULT 9
 ADR03370 standard; protein: 184 AA.
 ADR03370;
 AC XX
 XX
 DT 21-OCT-2004 (first entry)
 Human CD1a I-domain protein.
 CC CD1a antibody, human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; adult respiratory distress syndrome; allergic asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus (SLE); chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; human.

SLE; diabetes mellitus; Reinaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polyomavirus;
 KW chronic obstructive pulmonary disease; COPD;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy; human.

KW OS Homo sapiens.
 FH Location/Qualifiers
 FH Region 3..11 "Beta strand 1"
 PT /note= "Alpha helix 1"
 PT Region 19..34 "Alpha helix 1"
 PT Region 39..53 "Alpha helix 1"
 PT Region 57..62 "Beta strand 2"
 PT Region 67..71 "Alpha helix 2"
 PT Region 92..93 "Alpha helix 3"
 PT Region 105..112 "Alpha helix 4"
 PT Region 122..126 "Beta strand 3"
 PT Region 139..145 "Alpha helix 5"
 PT Region 142..151 "Beta strand 4"
 PT Region 160..163 "Alpha helix 6"
 PT Region 167..178 "Beta strand 5"
 PT Region 197..200 "Alpha helix 7"
 PN US2004146507-A1.
 PD 29-JUL-2004.
 PP 03-DEC-2003; 2003US-00727737.
 PR 27-NOV-1996;
 PR 20-NOV-1997;
 PR 97US-0031945P.
 XX (GUTH) GENENTECH INC.
 PR Jardieu PM, Prete LG;
 DR WPI: 2004-552640/53.
 PT New antibody mutant of a species-dependent antibody, useful for treating infectious diseases, seborrheic dermatitis, inflammatory bowel disease, preventing allergic conditions, autoimmune diseases, or cancer.
 XX Example: SEQ ID NO 7; 5pp; English.

CC The present invention relates to an antibody mutant of a species-dependent antibody with beneficial properties. The invention is useful for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reinaud's syndrome, immunological diseases such as chronic lymphocytic leukaemia; hairy cell leukaemia, graft versus host disease (COPD), CNS inflammation, polymyositis, and chronic obstructive pulmonary disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is human CD1a I-domain protein. This sequence is used in the exemplification of the invention.

SQ Sequence 184 AA;

Query Match Score 286.5; DB 8; Length 184;
Best Local Similarity 31.5%; Pred. No. 4.7e-23;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy | DIAFLIDSGSITPHFRMKEPVSTMDKSKTLLWQSERFHTPPEFONNP 66
Db 5 DLPVFLDKMSMLQDDEPKQIILDFMKYMKLANTSQYPAVAVOSSYKTEDEFDVYKVK 64

Qy 67 NPPSLVKPITPOLLCHRTATGKRVNWEELNTNGAARNPKLKVTDGSKEDDPLGYE 126
Db 65 DPDALAKHVKMMLMTNGAATVYVREBELLGARDATKVLIIIDGS- ATESGNI 122

Qy 127 DVPBPADREGVIVRIVLGVDADEPSEKSRGELATLIASTSPDHYFQVNNEFALLTQLR 186
Db 123 DAKD --- IIRVIGIGHOFQTKSQETLHKPASKPASBPVKTLDPEKLDLFTELQ 177

Qy 187 KX 188
Db 178 KX 179

RESULT 10
ADR23224 standard; protein; 187 AA.
XX ADR23224;
XX DT 04-NOV-2004 (first entry)
XX Human integrin CD11a alpha subunit A domain.
XX Human; integrin; CD11a; inflammation; antiinflammatory; vasotropics.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain /label = A_domain
XX Mbo-difference 182
XX /note= "Invariant Ile residue"
XX WO2004066914-A2.
XX 12-AUG-2004.
XX PD 76376
XX PP 12-MAY-2003 ; 2003WO-US014919 .
XX PR 10-MAY-2002 ; 2002US-00144259 .
XX (GRHO) GEN HOSPITAL CORP.
XX PI Arnaut MA, Li R, Xiong J;
XX DR WPI: 2004-593980/57.
XX GENBANK; AAC31672.

PT Novel variant integrin CD11b alpha subunit polypeptide, useful for determining compound as activation-dependent ligand.
XX Disclosure: SEQ ID NO 4: 128pp; English.
XX The present sequence is that of the human integrin alpha subunit CD11a A domain (amino acids 150-133 of the full-length protein). This includes an invariant Ile residue. The invention features variants of integrin alpha subunit polypeptides in which the invariant Ile is substituted by Gly, Ala or some other amino acid (e.g., Val) or is deleted. The polypeptide can include part or all of the A domain. Replacing the invariant Ile creates a variant integrin polypeptide that is more active (i.e., in solution has a greater proportion of ligand-forming polypeptides) than the wild-type form of the subunit. Variant integrin polypeptides of the

CC invention are useful in assays for compounds that bind to a variant ligand, that interfere with or enhance the binding of an integrin ligand to integrin, and for identifying activation-specific ligands. They are also useful for generating antibodies, e.g., monoclonal antibodies, which bind to the high efficiency conformation of an integrin. Some such antibodies recognise an epitope that is either non-existent or not accessible on an integrin that is in a lower affinity conformation. The invention also provides methods of administering a variant integrin polypeptide, or an antibody that selectively binds to a variant integrin which binds to an active integrin. Such assays are useful for diagnosing inflammation, e.g., occult inflammation (e.g., abscesses or active arteritis/cerebrovascular disease). A variant integrin polypeptide can also be used to test the bioavailability of a variant integrin polypeptide ligand and to treat disorders associated with atherosclerotic injury. A variant CD11a domain containing an Ile to Gly substitution was shown to display binding to the activation-dependent ligand ICAM-1 in a LISA assay. No binding was observed in the wild-type protein. Claimed polypeptides comprise: amino acids 150-131 of the CD11a alpha subunit sequence in which the Ile residue at position 131 is replaced by Gly or Ala; and amino acids 131-122 of the CD11a subunit but not amino acids 311-122 of CD11a.

CC XX Sequence 187 AA;

Query Match Score 286.5; DB 8; Length 187;
Best Local Similarity 33.0%; Pred. No. 4.8e-23;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;

Qy 1 CPQEDSDIAFLINGSGSIIIPHDFFRMKEFVSTMDKSKTLLFSLMOYSSEFRHIFTK 60
Db 1 CTKGNVQDVLVLFQGSMISQPEFKLDPMKVKKKUNTSOPFQAVQPSFSKTFKEDFS 60

Qy 61 EFPQNNPPIERLAVPPTQIOLGHTPATGKRVRELNFNTGKRNAPKILVUTDSEKKG 120
Db 61 DYVKKRQBDALIHKYHMLLNTPGAINVATVBFEREGARPDATVVLILITDGS-A 118

Qy 121 DPGYEDPDIYIPEAERSQWBYVTCUQGAFSEKPSQNSQVNTMKEPRDUFQEDNRAEAT 180
Db 119 TOSGRIDAAD-----IIRRIGVGRHAFQRESQTLHFKPASKPASPFVKTLDPEKLD 173

Qy 181 IONQLEK 188
Db 174 LPTELQKK 181

RESULT 11
ABB76376 standard; protein; 180 AA.
XX AC ABB76376;
XX DT 22-AUG-2002. (first entry)
XX DB Lymphocyte function associated antigen-1 domain.
XX KW Lymphocyte function associated antigen-1; LFA-1; human;
XX KW alpha/beta protein; ligand binding.
XX Homo sapiens.
XX OS Human.
XX PN WO200231511-A2.
XX PD 18-APR-2002.
XX PP 12-OCT-2001; 2001WO-US032047 .
XX PR 12-OCT-2000; 2000US-0239758P.
XX PA (ICOS) ICOS CORP .
XX P1 Stauton DE;
XX DR WPI: 2002-471361/50 .

XX Modulating binding interactions between alpha/beta proteins comprising an allosteric regulatory site, and a binding partner, by contacting with an allosteric effector molecule that interacts with the regulatory site.
 Disclosure: Fig 1, 163pp; English.

XX The present sequence is the protein sequence of the integrin (I) domain of lymphocyte function-associated antigen-1 (LFA-1). The invention provides methods of modulating the binding interaction of a first molecule, which is not LFA-1 or an I-domain-containing fragment of LFA-1, and a binding partner. The first molecule has an alpha/beta domain, a structure comprising an allosteric regulatory site. Modulation of the binding interaction involves contacting with an allosteric effector molecule that interacts with the regulatory site. In vivo methods are expected to alleviate and/or prevent pathological states arising from aberrant binding activity. Methods for identifying modulators are also provided.

XX Sequence 180 AA;

Query Match Score 282.5; DB 5; Length 180;
 Best Local Similarity 33.5%; Pred. No. 1.3e-22;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLDGSGSIIPHDPRMKPVSTVNEOLKSKTLEFSLWQYSBEPRIHPTKEFONNP 66
 Db 4 DLFVFLDPSMSMLOPDEFQKLDFMDYQMKLNLYSOPAVQFSTSYKTEPFDSDVYKHK 63

Qy 67 NPSILVKPITOLURHTHTGTRKVKBLVNTNGARNPKLIVVTDGKFEDPLGTYE 126
 Db 64 DPDALAKVHKMMLLTNTGANYVATEVREBLGARDATKYLILITDGS- ATDSGN 121

Qy 127 DVIPEADRGVIGRIVGVEDAIPRSKSRQLMTIASKEPDHYFQVNNEALKTIONQ 186
 Db 122 DAOKD---IRVIIQIGKHTQKESOOTHKFKASPKASBYKFLDKLDFEQ 176

RESULT 12
 AAY82350 ID AAY82350 standard; protein: 184 AA.

XX AC AAY82350;

XX DT 22-OCT-2000 (first entry)

DB Rhesus CD11a I-domain amino acid sequence SEQ ID NO: 8.
 XX Humanized; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; anti-tumour; antiviral; inflammation; immunological response; LFA-1; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
 XX Macaca mulatta.
 XX US6037454-A.
 PN XX
 XX 14-MAR-2000.
 PD XX
 KW 20-NOV-1997; 97US-00574899.
 PP XX
 PR 27-NOV-1996; 96US-0031971P.
 PA (GENTECH INC.
 Jardieu PN, Presta LG:
 DR WPI: 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g. PR inflammation and transplant rejection, contains human heavy variable PR region complementarity determining regions.
 XX PS Example: Fig 2, 38pp; English.

XX The present invention describes a humanized anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1) which is involved in leukocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (i) opsonization when coupled to a cyclocon, (ii) target or prevent disease mediated by lymphocyte function-associated antigen (LFA-1), CD11a/CD11b, e.g. seborrheic, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukemia, viral infections and many others; also for: (iii) inhibiting graft rejection; (iv) when linked to detect CD11a; (v) for tumour prevention; (vi) for delivery of enzymes that convert products to active anticancer agent; and (v) for affinity chromatography. The Ab retains about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which it is derived. The murine anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion between Jurkat cells expressing LFA-1 and normal epithelial keratinocytes that express ICAM-1 (intracellular adhesion molecule-1). The fully humanized version of MHM24 had IC50 0.13 nM. The present sequence represents the amino acid sequence of the rhesus CD11a I-domain, which is used in the exemplification of the present invention.

XX Sequence 184 AA;
 SO Query Match Score 29.2%; DB 3; Length 184;
 Best Local Similarity 33.0%; Pred. No. 1.7e-22;
 Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;
 Qy 7 DIAPUDGSSSIIPHDPRMKPVSTVNEOLKSKTLEFSLWQYSBEPRIHPTKEFONNP 66
 Db 5 DLJLFQGNSMSLQDPSFQKLDPFKQYMKLNTSYQFAAVOFSTSYKTSDFDIDVYKOK 64
 Qy 67 NPRLSLVKPITOLURHTHTGTRKVKBLVNTNGARNPKLIVVTDGKFEDPLGTYE 126
 Db 65 DPDALAKVHKMMLLTNTGANYVATEVREBLGARDATKYLILITDGS- ATDSGN 122
 Qy 127 DVIPEADRGVIGRIVGVEDAIPRSKSRQLMTIASKEPDHYFQVNNEALKTIONQ 186
 Db 123 DAOKD---IRVIIQIGKHTQKESOOTHKFKASPKASBYKFLDKLDFEQ 177
 Qy 187 EK 188
 Db 178 KK 179

RESULT 13
 AD538996 ID AD538996 standard; protein: 184 AA.
 KW XX
 AC AD538996;
 KW XX
 DT 26-FEB-2004 (first entry)
 XX DB Monkey CD11a I-domain.
 KW XX
 KW Monkey; CD11a; I-domain; monoclonal antibody;
 KW cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; prodrug activating enzyme.
 OS XX
 OS Macaca mulatta.
 PN XX
 PN US2003207336-A1.

disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is Rhombus macaque CD11a I-domain protein. This sequence is used in the exemplification of the invention.

Sequence 184 AA:

```
29 21; Score 281.5; DB 8; Length 184;
CC Query Match Best Local Similarity 31.0%; Pred. No. 1.7e-22; Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;
CC
CC 65 DPDALERKMLLNTFGAINTVATVERBLKLARDKVKLILRDTG-
CC
CC 127 DIVPSADRGVIRTVIGQDARPSKGQRLAATIASKEPDHYFQVNINFALKTQR 186
CC
CC 123 DAAD----ITRVIGICKHFTKESQSTLHKFASKPASEBPKLDTFLDQ 177
CC
CC 187 KK 188
CC
CC 178 KK 179
```

RESULT 15

ID AAU76848 standard; protein: 184 AA.

XX

XX

AC AAU76848;

XX

DT 21-MAY-2002 (first entry)

XX Human integrin alpha subunit CD11a domain.

XX Human; integrin alpha subunit; A domain; CD11a; integrin beta subunit;

XX A-like domain; inflammatory disorder; skeletal muscle injury; reticulosis;

XX ischaemia-reperfusion injury; immune complex; parasitic disease;

XX antiinflammatory; vasoconstrictor; vasoconstrictive; vasoconstrictive;

XX Homo sapiens.

XX Key Location/Qualifiers

XX 1..181 *This region is specifically claimed*

XX /note= "This region is specifically claimed"

XX WO200209737-A1.

XX PD 07-FEB-2002.

XX 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-0221950P.

PR 11-JAN-2001; 2001US-00758493.

PR 13-MAR-2001; 2001US-00005354.

XX (GERO) GBN HOSPITAL CORP.

XX Arnault AM, Li R, Xiong J;

XX WPI; 2002-188567/24.

XX Novel high affinity integrin polypeptide useful for treating restenosis

XX and parasitic diseases; comprises all or part of variant integrin alpha

XX subunit A domain or variant integrin beta subunit A-like domain.

XX Example 2, Fig 5; 55pp; English.

XX The invention relates to a high affinity integrin polypeptide comprising

all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 312 has been replaced by C, or G or A, P at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemia-reperfusion injury, immune complexes, retenocones and parasitic diseases, two hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit CD11a domain.

Sequence 184 AA:

```
Query Match Score 281.5; DB 5; Length 184;
CC Best Local Similarity 33.0%; Pred. No. 65-22; Matches 67; Gaps 2;
CC Matches 67; Conservative 48; Mismatches 71; Indels 7; Gaps 2;
CC
CC 1 CPGEDIAALIGGSSSIPRDPKPKRPTSPQMKRSKTLPSLWQYSEPRFLPK 60
CC
CC 1 CTKGNVOLVLFQGMSNQDPEQLDFMDVKLQNSTSQAVGFTSKTFDF 60
CC
CC 61 BFQNNPNPFRSLVPLKPTQOLGRTHTAGIRKVRVLEFTINGARKAFLILVVTQDKKG 120
CC
CC 61 DRYKNDPDLAKHXRHMLUTNIFAINYATEFREBLGARDPATKLJLTDGB--A 118
CC
CC 121 DPLGYTBVTPIDPREGCVTRVIGDAAFSBSBHQELNTASPPDVIVPQVNFEALKT 180
CC
CC 119 TDSGNIDAD----IIRRIGLGKHFQTKESQTHPKSPKASBEVKKLDTFEKLKD 173
CC
CC 161 IONQLRK 188
CC
CC 174 LTFEQQK 181
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Search completed: November 14, 2005, 17:34:35

Job time : 165 sec(s)

A:Cross-references: UNIPROT:O27130; GB:AE000876; GB:AB000666; PID:92622140; PIDN:AAE	C:Cross-references: UNIPROT:O27130; GB:AE000876; GB:AB000666; PID:92622140; PIDN:AAE
A:Experimental source: strain Delta H	
A:Genetic: MTH1056	C:Superfamily: ribosomal protein S7/SS
A:Genetic: A/B/C/D/E/F/G/H/I/J/K/L/M/N/O/P/Q/R/S/T/U/V/W/X/Y/Z	
Qy RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63	Qy RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63
Qy Best Local Similarity 22.1%; Pred. No. 46; Mismatches 36; Conservative 29; Indels 52; Gaps 53; B;	Qy Best Local Similarity 22.1%; Pred. No. 46; Mismatches 36; Conservative 29; Indels 52; Gaps 53; B;
Db 16 EDEGLAKYICLDSLIVPHTMGR----HYRQEPAKSRY-----18	Db 16 EDEGLAKYICLDSLIVPHTMGR----HYRQEPAKSRY-----18
Qy 64 NYPNPNSRLSVEKPTTOLGLRTGATGIR----KVRELENITIN-GARNNAFKILVYTIDGG-E-117	Qy 64 NYPNPNSRLSVEKPTTOLGLRTGATGIR----KVRELENITIN-GARNNAFKILVYTIDGG-E-117
Db 49 -----SVBLLINKWARTENSGEKAYKVAQAFLLINRTPVQLIVAVENTS 102	Db 49 -----SVBLLINKWARTENSGEKAYKVAQAFLLINRTPVQLIVAVENTS 102
Qy 118 -----KGDPGLVKE--DPIVFEADRGCVYVY---GIVGDAPREKGROE 156	Qy 118 -----KGDPGLVKE--DPIVFEADRGCVYVY---GIVGDAPREKGROE 156
Db 103 PRBTETRKYGG-IGYQAVADISQRVVDISLGPITRGQAQFAFKRSKIBS 153	Db 103 PRBTETRKYGG-IGYQAVADISQRVVDISLGPITRGQAQFAFKRSKIBS 153
RESULT 5	
RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63	RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63
hypothetical protein aq_2028 - Aquifex aeolicus	
C:Species: Aquifex aeolicus	C:Species: Aquifex aeolicus
C:Accession: B70474	C:Accession: B70474
V. Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.	V. Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998	Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus	A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A:Reference number: A0300; PMID:9196666; PMID:537320	A:Reference number: A0300; PMID:9196666; PMID:537320
A:Accession: B70474	A:Accession: B70474
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown	A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Gene: A; A:Note(s) type DNA	A:Gene: A; A:Note(s) type DNA
A:Cross-references: UNIPROT:O67822; GB:AE000766; PID:92984245; PIDN:AAE	A:Cross-references: UNIPROT:O67822; GB:AE000766; PID:92984245; PIDN:AAE
C:Experimental source: strain VF5	C:Experimental source: strain VF5
RESULT 6	
RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63	RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63
hypothetical protein Af1244	
Query Match 7.4%; Score 71.5; DB 1; Length 169;	Query Match 7.4%; Score 71.5; DB 1; Length 169;
Best Local Similarity 23.5%; Pred. No. 50; Mismatches 56; Indels 35; Gaps 6;	Best Local Similarity 23.5%; Pred. No. 50; Mismatches 56; Indels 35; Gaps 6;
Matches 36; Conservative 24; Indels 35; Gaps 6;	Matches 36; Conservative 24; Indels 35; Gaps 6;
Qy 14 GSQSPKIPIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQNNPNPSS--70	Qy 14 GSQSPKIPIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQNNPNPSS--70
Db 29 GSQSPKIPIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQNNPNPSS--70	Db 29 GSQSPKIPIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQNNPNPSS--70
Qy 71 LYKPI-----TOLGIHTATGCKVYRFLNTINGARKNAFKILVYTIDGGFG 120	Qy 71 LYKPI-----TOLGIHTATGCKVYRFLNTINGARKNAFKILVYTIDGGFG 120
Db 87 LAKETVMMWVKVGSNSNFIGTSDLDIR-----RKTGVSTIAIIRDGMETP 133	Db 87 LAKETVMMWVKVGSNSNFIGTSDLDIR-----RKTGVSTIAIIRDGMETP 133
Qy 121 DPLGYEDVWPEAD-----REGVYVIGVGD 146	Qy 121 DPLGYEDVWPEAD-----REGVYVIGVGD 146
Db 134 SPPDYKPKIQGQYLVVCTBOLIKEFLMCD 166	Db 134 SPPDYKPKIQGQYLVVCTBOLIKEFLMCD 166
RESULT 6	
RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63	RTDIAPIFICGSSITIPIIDPRMKEPVSTVMSQKSLKSTPSLMSQESEPRHIFTPEKFQ 63
hypothetical protein MJ0063 - Methanococcus jannaschii	
C:Species: Methanococcus jannaschii	C:Species: Methanococcus jannaschii
C:Accession: G61307	C:Accession: G61307
J. S. Sadow, P.T.W.; Hanne, M.C.; Coton, M.D.; Roberts, K.M.; Hurst, M.A.; Merrick, J.M.; Glodck, P.; Reich, C.I.; Overbeck, M.J.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Jannasch, H.W.; Sloss, J.D.; Sutton, G.J.; Kirchner, E.P.; Weineck, K.G.; Blaier, J.; Blaier, C.; Reich, C.I.; Kaine, B.P.; Borodovskiy, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Jannasch, H.W.	J. S. Sadow, P.T.W.; Hanne, M.C.; Coton, M.D.; Roberts, K.M.; Hurst, M.A.; Merrick, J.M.; Glodck, P.; Reich, C.I.; Overbeck, M.J.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Jannasch, H.W.; Sloss, J.D.; Sutton, G.J.; Kirchner, E.P.; Weineck, K.G.; Blaier, J.; Blaier, C.; Reich, C.I.; Kaine, B.P.; Borodovskiy, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Jannasch, H.W.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii	A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A0300; PMID:9196666; PMID:537320	A:Reference number: A0300; PMID:9196666; PMID:537320
A:Accession: G61307	A:Accession: G61307
A:Status: Draft genome	A:Status: Draft genome
A:Gene: A	A:Gene: A
A:Cross-references: UNIPROT:O67822; GB:AE000766; PID:92984245; PIDN:AAE	A:Cross-references: UNIPROT:O67822; GB:AE000766; PID:92984245; PIDN:AAE

```

SUIT 8
H62860 Protein S12 UWS25 [imported] - Ureaplasma urealyticum
Species: Ureaplasma urealyticum
Date: 1-Aug-2000 #text_change 20-Aug-2000 #text_change 12-Jun-2003

RESULT 10
H69159 Hypothetical protein MTH458 - Methanobacterium thermoautotrophicum (strain Delta H)
C.Species: Methanobacterium thermoautotrophicum
C.Date: 05-Dec-1997 #Sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C.Accession: H69159
R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,

```

i: Olu, D.; Spadafora, R.; Vilcaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Kirki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.; J. Bacteriol. 179 : 7155-7155 ; 1997 .

A; Status: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H; function: A; Reference number: A95000; MID:98337515;; PMID:9371443

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecular type: DNA

A; Residues: 1-10 <MTH>

A; Cross-references: UNIPROT:OP6558; GB:AE000830; GB:AE000666; PIDN:AAB8496

A; Experimental source: strain Delta H

A; GenBank accession: MTH458

Qy: REICH, C.I.; Overbeek, R.; Kirkness, S.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, M.; Carlson, J.D.; Sadow, P.W.; Hanra, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 271 : 1088-1093 ; 1996

A; Authors: Kaine, B.P.; Borodovsky, M.; Klein, H.P.; Fraser, C.M.; Smith, H.O.; woebe G; Reference number: A64300; MID:9317999; PMID:6768087

A; Title: Complete Genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*

A; Accession: A64300

A; Status: Preliminary; nucleic acid sequence not shown; translation not shown

A; Molocule type: DNA

A; Residues: 1-175 <MTH>

A; Cross-references: UNIPROT:Q57692; GB:U67479; GB:L77117; NID:91590965; PIDN:AAB98225

C; GenBank accession: A64300

A; Gene: MTH458

Qy: REV21618-231091

C; Superfamily: Thermophilic adenylyl cyclase, CyaB type

Qy: Query Match 7.1%; Score 68.5%; DB 2; Length 30;

Db: Best Local Similarity 23.8%; Pred. No. 41; Matches 24; Conservative 16; Mismatches 30; Indels 31; Gaps 5;

Qy: 1 CPOEDSIAFLDGSSTIIPHDPRMKEPVSTMSLQLKSTPSMQLMSPRHTPK 60

Db: 13 CDAEPTV---GATEIL---DADTVT---KCKLRGSDNYRAI----- 49

Qy: 61 EPNONPNPRLVKPITOLGLGRHTATGIRKVWPLRFNITNG 101

Db: 50 -PENRAT-----PAITDREWNITNRVPREFLGVDGG 82

RESULT 11

Qy: 13824 centrin - human

C; Species: Homo sapiens (man)

C; ID: Baro - 1998 Sequence_revision 29-May-1998 #text_change 09-Jul-2004

C; Accession: 13824

R; Substrat: R.; Sanders, M.N.; Salisbury, J.L.

J; Cell Sci.: 107 : 919-16, 994

A; Title: Cloning of a cDNA encoding human centrin, an EF-hand protein of centrosomes and microtubules

A; Accession: 138424

A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molocule type: mRNA

A; Residues: 1-172 <RES>

A; Cross-references: UNIPROT:Q12798; EMBL:001270; PIDN: AAC27343.1; PID:9414

C; Superfamily: calmodulin repeat homology

C; Keywords: EF hand

P; 21-50 /Domain: calmodulin repeat homology <EF1>

P; 64-96 /Domain: calmodulin repeat homology <EF2>

P; 101-131 /Domain: calmodulin repeat homology <EF4>

P; 137-165 /Domain: calmodulin repeat homology

Qy: 13824 centrin - human

Db: Best Local Similarity 25.6%; Pred. No. 1..1e+02; Matches 31; Conservative 25; Mismatches 54; Indels 17; Gaps 6;

Qy: 10 PLIDSGSLPHFRMKPEPVSTMSLQLKSKTLFSLMQLKSEPRHTPKFSQNPNP 69

Db: 40 PVDGSGTI---DKAKELTYVYHARGFPRKEKOMKISVEWDRGKTKISPNDP----- 89

Qy: 70 SLVKEPTOLGLGRHTATGIRKVWPLRFNITNGARNAKFLVVTID-GKPGPQYGD 127

Db: 90 -LAVPTQSEKCTREEELKARY-LD-DDETGKISPKNIKVANEGLMTB-ELQE 144

Qy: 128 VIDEADR 136

Db: 145 MIDEADR 153

RESULT 12

A64300 hypothetical protein M0240 - Methanococcus jannaschii

C; Species: Methanococcus jannaschii

C; Date: 13-Sep-1996 Sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

A; Accession: A64300

R; Built: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

Qy: 93 RELENITNGARNAKFLVVTID-GKPGPQYGD 135

Db: 59 GRFFTYRKGKIDKISKTRBIEVTKEDBRKRQRQPKLGKPFVPPRKIRBYKGKD 118

Qy: 136 GVTRVIGVQDADPFSRSKRSRNTIASPKRDPHYPOVNNSBALKT 181

Db: 119 ASIDDVEDALFPLEKSIDIN-----EKDVKLB-EMMETKLK 157

RESULT 13

C; Species: Rickettsia prowazekii

C; ID: Baro - 1998 Sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C; Accession: C71706

C; Description: Rickettsia prowazekii

R; Anderson, S.G.E.; Zorododipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alemark Nature 395 : 121-140, 1998

A; Title: The Genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A; Accession number: A11530; MID:9303439; PMID:9833893

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Accession: C71706

A; Molocule type: DNA

A; Residues: 1-150 <AND>

A; Cross-references: UNIPROT:Q9ZD74; GB:AJ235271; GB:AJ235269; NID:93868717; PIDN:CAAL

C; Genetics:

C; Superfamily: Rickettsia prowazekii hypothetical protein RP470

Qy: 93 RELENITNGARNAKFLVVTID-GKPGPQYGD 135

Db: 58 YONKSTPSPLEPFTSLKDHEKAA-RSVIKHLKVT-ANDAKYKLIIIAEPMQG 114

RESULT 14

A95901 uncharacterized conserved protein, ortholog of *VXVA* B. subtilis CAC0009 [imported]

C; Species: Clostridium acetobutylicum

C; ID: Baro - 14-Sep-2001 Sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C; Accession: A95901

R; Rolling, J.; Beacon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; i

J; Daly, M.J.; Bartram, G.; Koontz, E.V.; Smith, D.R.

J; Bacteriol. 183 : 4837-4838 ; 2001

A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A; Reference number: A95901; MID:21353325; PMID:121353325

A; Accession: A95901

A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-171 <KUR>
 A; Cross-references: UNIPROT:Q97N29; GB:AE001437; PID:AAK77996.1; PID:gi1502827; GSPPDB:Q
 A; Experimental source: Clostridium acetobutylicum ATCCB24
 C; Genetics:
 A; Gene: CAC0009

Query Match Similarity 6.9%; Score 67; DB 2; Length 171;
 Best Local Similarity 22.5%; Pred. No. 1.2e+0; Gaps 6;
 Matches 38; Conservative 23; Mismatches 72; Indels 36; Gaps 6;

Qy 50 SREPRINPTPKERONNNP-----RSLVKPTITOLGRHTATGIRKVREL 95
 Db 3 SBERENNIKIK-LENDDEPIKGSTLAREGYTRQVTKDIAILRAKGHKTKATPGCY -- 59
 Qy 96 PPTINGARKKAAPF-ILVVVITDGKEKEFDPLG-----RYVYTGCD 146
 Db 59 --INNKNSNSIKRVLAVERNAIDELNSVTKGCVDTYEDVIEHPLGERGILMIRT 116
 Qy 147 AFRSEKSRQELNTTASXP-----PFRHVFQVNNEFAKTNQNLREK 188
 Db 117 LFDPVKMFNKKIRDYSAEFLSILTGWHIITRDNEDNNIVDELTRK 165

RESULT 15

H5433
 hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Accession: H5433
 C;Date: 03-Dec-1999 #Sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.J.;
 S.M.; Shen, M.; Vamathevan, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 26, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MNUD:20016396; PMID:10567266
 A;Accession: H5433
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-126 <PHI>
 A; Cross-references:
 A; Experimental source: strain R1
 C; Genetics:
 A; Gene: DR121
 A; Map position: 1

Query Match Similarity 6.8%; Score 66; DB 2; Length 126;
 Best Local Similarity 27.0%; Pred. No. 1e-02; Gaps 6;
 Matches 34; Conservative 18; Mismatches 50; Indels 24; Gaps 6;

Qy 80 QRTTH-----ATGIRKVPELFNTNGARAKNAPKLLVYTGDKKFGDPPLGVEDVIREAD 133
 Db 6 GRHHTHEPITRASHWV-VDQVFLARQRLIEVCSLV----NDRGGDLRHHSVATDD 60
 Qy 134 REGV-----RYVYTGCDAF-----RSBSKSOBLINTIASPPRD---HVPQVNNEFEALKT 180
 Db 61 PAQQRVRAHARFYAGKGNVFSARNAVWRAREQLTTQDPLRDTLDFTPQEFEETLAA 120
 Qy 181 IONQLR 186
 Db 121 VRDLR 126

Search completed: November 14, 2005, 17:38:17
 Job time : 40 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	November 14, 2005, 17:05:43 : Search time 172 Seconds protein - protein search, using sw model on on:	US-09-758-493-1_COPY_1_188 Title: Effect score: 965 Protein target: 1 cronobacter tocsoicidin Protein source: 1 cronobacter tocsoicidin
Q6XKU1	Pseudomonas aeroplana	32	70
Q9PWW5	Rickettsia rickettsiae	33	69.5
OPB813	O2HQS2	34	69.5
Q92HQ9	Parachlamydia	35	69.5
Q6M443	Methanococcus	36	69
Q6LYPS	Staphylococ	37	69
QBYL19	Methanobacte	38	69
Q26558	Escherichia	39	68.5
Q8ZV59	homo sapien	40	68.5
Q6ZV59	rickettsia	41	68.5
Q6B9R0	drosophila	42	68.5
P4955B	homo sapien	43	68.5
Q6ZQX1	covillei	44	68.5
Q26554	homo sapien	45	68.5

searched: 1612378 seqs, 512079187 residues

searched: 1612378 seqs, 512079187 residues

Archived : 1612378 seqs, 512079187 residues

RESULT 1

RESULT 1

RESULT 1

RESULT 1

base : UniProt_03.
 1: uniprot_sprot:
 2: uniprot_trembl:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Uniprot_03:
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred_No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

אדרת אגדות

RESULT	2	QBYK41	PRELIMINARY;	PRT;	79 Å.
ID	QBYK41				
AC	QBYK41;2				
DT	01-MAR-2003	TREMBEL1	23	Created)	
DT	01-MAR-2003	TREMBUR1	23	Last sequence update)	
DT	01-OCT-2003	(TREMBUR1	25	Last annotation update)	
DB					
LA	Leucocyte integrin alpha-M				
NN	Name=dlib				
OB	Bos Taurus (Bovine)				
OC	Bukaryota				
OC	Eukaryota; Metazoa;				
OC	Chordata; Craniata; Vertebrata; Buteleostomi;				

RESULT	2
Q8HY41	
ID	Q8HY
AC	Q8HY
DT	01-M
DT	01-M
DT	01-O
DB	Leuk
GN	Name
OS	Bos
OC	Euka

OX [1] _TAXID=272560;	59	TWKDYMPQVRKRAIRAKKGATAAVREVCAASFGANYAMREWFEKTPKGPGTPE	118
RN [1] _FROM N.A.			
RP SEQUENCE FROM N.A.			
RC STRAIN=K06243;			
RA Pubmed=1537794;			
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,			
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,			
RA Bentley S.D., Sebastian M., Thomson N.R., Basin N., Beacham I.R.,			
RA Brooks K., Brown K.A., Brown N.F., Charlis G.L., Cherevach I.,			
RA Chillingworth T., Cronin J., Crosson B., Davis P., Deshafer D.,			
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,			
RA Keith K.E., Maddison M., Monle S., Price C., Quail M.A.,			
RA Songkviatlai S., Stevens K., Tompkins K., Vesarachaveet M.,			
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.P., Parkhill J.,			
RT "Genomic Plasticity of the causative agent of melioidosis,"			
RT Burkholderia pseudomallei,"			
RT Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).			
DR EMBL: BX71661; CNAH38561; 20280 Km;			
DR NCBI_TAXID=221986;			
SEQUENCE 184 AA;			
Query Match 8.5%; Score 82; DB 2; Length 184;			
Best Local Similarity 28.4%; Pred. No. 74; Indels 16; Gaps 4;			
Matches 29; Conservative 15; Mismatches 42;			
Qy 58 TPKFEPNNPFRSLSVKPTQLGTTNGIRKV-----VRELNTNGARRNAPK	108		
Db 59 TWKDYMPQVRKRAIRAKKGATAAVREVCAASFGANYAMREWFEKTPKGPGTPE	118		
Qy 109 ILVVITDQEKGDPGLYE---DVIPEADR--EGVTRIVIGVG	145		
Db 119 ILMVY-GARDGTPATAEVADIAEVDAKRGTAHYTFQG	158		
RESULT 6			
ID 063194	PRELIMINARY;	PRT;	184 AA.
AC AC_063194;			
DT DT 25-OCT-2004 (TREMBrel. 28, Created)			
DT DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)			
DT DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)			
DB Putative Page Protein.			
GN ORFNAMES=BPLO15;			
OS Burkholderia pseudomallei K96243.			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC Burkholderiales; Burkholderiidae.			
NCBI_TAXID=272560;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=K06243;			
RA Pubmed=1537794;			
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,			
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,			
RA Bentley S.D., Sebastian M., Thomson N.R., Basin N., Beacham I.R.,			
RA Brooks K., Brown K.A., Brown N.F., Charlis G.L., Cherevach I.,			
RA Chillingworth T., Cronin J., Crosson B., Davis P., Deshafer D.,			
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,			
RA Keith K.E., Maddison M., Monle S., Price C., Quail M.A.,			
RA Rabinowitz B., Rutherrford K., Sanders M., Simmonds M.,			
RA Songkviatlai S., Stevens K., Tompkins K., Vesarachaveet M.,			
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.P., Parkhill J.,			
RT "Genomic Plasticity of the causative agent of melioidosis,"			
RT Burkholderia pseudomallei,"			
RT Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).			
DR EMBL: BX71665; CNAH3401;			
SEQUENCE 184 AA;	20250 Km;	SOC09A7706078B2 CRC64;	
Query Match 8.5%; Score 82; DB 2; Length 184;			
Best Local Similarity 28.4%; Pred. No. 74; Indels 16; Gaps 4;			
Matches 29; Conservative 15; Mismatches 42;			
Qy 58 TPKFEPNNPFRSLSVKPTQLGTTNGIRKV-----VRELNTNGARRNAPK	108		
Db 59 TPKFEPNNPFRSLSVKPTQLGTTNGIRKV-----VRELNTNGARRNAPK	108		
RESULT 7			
ID 065WPS	PRELIMINARY;	PRT;	153 AA.
AC AC_065WPS;			
DT DT 25-OCT-2004 (TREMBrel. 28, Created)			
DT DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)			
DT DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)			
DB Hypothetical protein.			
GN ORFNAMES=MS008;			
OS Mannheimia succiniciproducens MBBL55E;			
OC Pasteurellales; Gammaproteobacteria; Pasteurellales;			
OC OC			
NCBI_TAXID=221986;			
RN [1]			
RP STRAIN=MBBL55E;			
RC RA			
RA Kim S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,			
RA Kim C.-H., Jeong H., Hur C.-G., Kim J.-G.,			
RT *The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens,"			
RT Nat. Biotechnol. 18:1682; AAC036705.1;			
DR DR			
KW HYPOTHETICAL PROTEIN; 0.0-0 (2004).			
SEQUENC 153 AA;	17160 MW;	'74742FOCDODC3F7B CRC64;	
Query Match 8.4%; Score 81; DB 2; Length 153;			
Best Local Similarity 31.2%; Pred. No. 73; Indels 16; Gaps 7;			
Matches 34; Conservative 20; Mismatches 20;			
Qy 22 DFRAKISGVSTYMEOLRSKTSKFLSLMVSSEPF-VIHTPKEFONNPNSRLVKTQILG	80		
Db 22 DFRAKISGVSTYMEOLRSKTSKFLSLMVSSEPF-VIHTPKEFONNPNSRLVKTQILG	80		
Qy 8 DPGAKVKE-LGSVAQKAPRFLALL--GEBUNKHHDIFRKTEKQPNG---RPWTPLAA	60		
Db 8 DPGAKVKE-LGSVAQKAPRFLALL--GEBUNKHHDIFRKTEKQPNG---RPWTPLAA	60		
Qy 91 PRHHTATGIR---KVYRELLETFNGARKRANKLIVVITGEGKFDGPGLGY	125		
Db 91 KVHHTATGIR---KVYRELLETFNGARKRANKLIVVITGEGKFDGPGLGY	125		
Qy 61 KTLLAKRKGSKLSLTIQDGNLN--KTAVNL--DDOVEFGSPKVY	103		
Db 61 KTLLAKRKGSKLSLTIQDGNLN--KTAVNL--DDOVEFGSPKVY	103		
RESULT 8			
ID Q749A4	PRELIMINARY;	PRT;	162 AA.
AC AC_Q749A4;			
DT DT 05-JUL-2004 (TREMBrel. 27, Created)			
DT DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)			
DT DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)			
DB Ribosomal protein S5.			
GN Name=sps; OrderedLocusNames=SGU2840;			
OS Bacteries; Sultureducens; Geobacteraceae; Geobacter.			
OC OC			
NCBI_TAXID=35554;			
RN [1]			
RP SOURCE: FROM N.A.			
RC STRAIN=PCA / ATCC 51573;			
RA PubMed=14611304; DOI=10.1126/science.1088727;			
RA Merhe B.A., Nelson K.B., Biesen J.A., Paulsen I.T., Nelson W.C.,			
RA Heidelberg J.P., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,			
RA Madupuri R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,			
RA Gwyn M.L., Kolonay J.F., Sullivan S.A., Huff D.H., Salengro J.,			
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,			
RA Weidman J.P., Khouri H.M., Reichly T.V., Utterback T.R.,			
RA Van Aken S.B., Lovley D.R., Frazer C.M.,			
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface environments";			
RA Science 305:1967-1969 (2003).			
RR -1- SIMILARITY: Belongs to the ribosomal protein SSP family.			
CC CC			

RESULT 15	QLTV3	PRELIMINARY:	PTT:	135 AA.
	Q6TRV3			
	Q6TRV3	TREMBL1: 27, Last sequence update		
	Q6TRV3	TREMBL1: 27, Last sequence update		
	Q6TRV3	TREMBL1: 27, Last sequence update		
	Q6TRV3	Hypothetical protein.		
	Q6TRV3	Order=locusNames=PPRA0059		
	Q6TRV3	Photobacterium profundum (Photobacterium sp. (strain SS9))		
	Q6TRV3	Bacteria: Proteobacteria: Gammaproteobacteria: Vibrionales: Vibrionaceae: Photobacterium.		
	Q6TRV3	NBII_TaxID:74109,		
	Q6TRV3	[1]		
	Q6TRV3	SEQUENCE FROM N A		
	Q6TRV3	VITILO N., LAURO F.,		
	Q6TRV3	CAMPANARO S., D'ANGELO M., SIMONATO B., CANNATA N., BARTLETT D.,		
	Q6TRV3	CESTARI A., MALARDA G., SIMONATI B., CANNATA N., BARTLETT D.,		
	Q6TRV3	VALLE G.		
	Q6TRV3	"Genome analysis of photobacterium profundum reveals the complexity of		


```

RESULT 2
US-0-687-706-61 Application US/08687706
; Sequence 61, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS: 62
; ADDRESSEES: Paired L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentNet Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/177,109
; PUBLISH DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Paetz, Peter L.
; REGISTRATION NUMBER: 31,284
; REREFERENCE DOCKET NUMBER: WU 107 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8994
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TIPS: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

US-0-687-706-61

Query Match 99.5%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 3-4e-96;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CP0B0D1A01DGS1LPH0PFRMKEVSTMELAKSTLS1MQSSEPF1HPTFK 60
1 CP0E0D1A01DGS1LPH0PFRMKEVSTMELAKSTLS1MQSSEPF1HPTFK 60
1 BPNQNNPRSPSLKPTGKPTOLGLRTATGIRKVRLEFTNTGARNAKFLKVITDGEKFG 120
1 EPQNNPRSPSLKPTGKPTOLGLRTATGIRKVRLEFTNTGARNAKFLKVITDGEKFG 120
1 DPLGKEDP1EPADEGTCUTVIGCDARPEKSROQLT1ASKPDRHDFQVNNEALKT 180
1 DPLGKEDP1EPADEGTCUTVIGCDARPEKSROQLT1ASKPDRHDFQVNNEALKT 180

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RESULT 3
US-08-177-109A-62
Sequence 62 Application US/08177109A
Patent No. 6,868,815
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASSS
NUMBER OF SEQIDS: 62
CORRESPONDENCE ADDRESS: P. O. Box 1, Pabst
ADDRESSSES: Patrecia L. Pabst
STREET: 2800 One Atlantic Center
CITY: 1201 West Peachtree Street
STATE: Georgia
COUNTY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEX: (404) 873-8795
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-177-109A-62

Query Match Score 534; DB 2; Length 187;
Best Local Similarity 55.3%; Pred. No. 5.4e-50;
Matches 104; Conservative 34; Mismatches 44; Indels 0; Gaps 0;
Qy 1 CPROSDIAPISGSGTIPDPRMKESITVMEQLSKSTLFSIMOVSSEFRHTFK 60
Db 1 CPROSDIPLIGSSISSNATGNNTRAVISOFRPSTFSIMOFNSKFRHTFP 60
Qy 61 EFRPNPSNLSSVHOLQGETATIQVHRLFHSYGARDKTLIVTDGKEG 120
Db 61 EFRPSNLSSVHOLQGETATIQVHRLFHSYGARDKTLIVTDGKEG 120
Qy 121 DPGEDVDTIPRDPREGVRYTGHDAPESEKSRDLATIASKPDDHFOVNNPBALKT 180
Db 121 DSQDKDTPMDAGITRAAGLAFQTRASWKLNDIASPQEHEFRTEDPDALKD 180
Qy 181 IONQRS 187
Db 181 IONQLRS 187

RESULT 4
US-08-687-706-62
Sequence 62 Application US/08687706
Patent No. 5,928,832
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby

```

TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS: Pabst, Parrea L.
 STREET: 1201 West Peachtree Street
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/08/687,706
 FILING DATE: 26-JUL-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/177,109
 FILING DATE: 03-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Parrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: WU 107 DIV
 TELEPHONE: (404) 873-8794
 TELEFAX: (404) 873-8795
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCES CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US-08-687-706-62

Query Match 55.3%; Score 534; DB 5; Length 187;
 Best Local Similarity 55.6%; Prod No. 5.4e-50;
 Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPQDSIALIDGGSSTIIPHDFRANKPEFTMELQKKSFLSLMQSEFRHHTPK 60
 Db 1 CPQDGVIPFADRGIVTVIGDIAFRSKSPRLANTASKPRDRHQVNINFBAKLT 180

Qy 61 EPQNPPRLYKPTQLGRTHAARGKVRFLNITGARNQAKLIVTQEGF 120
 Db 61 EPRTSPSLIASHQLOQFTTATAQVHRLPHASYGRDQTFB 60
 Db 121 DPLGEVIFPDRGIVTVIGDIAFRSKSPRLANTASKPRDRHQVNINFBAKLT 180

Qy 121 DPLGEVIFPDRGIVTVIGDIAFRSKSPRLANTASKPRDRHQVNINFBAKLT 180
 Db 121 DSQDVKIPMDAIGTRIAVQGVLAFQNRNSKELNDIASKPSQHFKVEDFDALKD 180

Qy 181 IONOLRE 187
 Db 181 IONOLKE 187

RESULT 6
 US-09-758-493-1_copy_1_188.raii
 Sequence 7, Application US/08974899
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; ATTORNEY: Jardiu, Paula M.
 ; TITLE OF INVENTION: Humanized Anti-CD1a Antibodies
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPat in (Genentech)
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974, 899
 FILING DATE: 08/08/974, 899
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 FILING DATE: 11/27/96
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 60/031971
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/255-9881
 TELFAX: 650/932-9881
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLogy: Linear
 US-08-974-899-7

Query Match 29 7%; Score 286.5; DB 3; Length 184;
 Best Local Similarity 33.3%; Pred. No. 3.6e-23; Gaps 2;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
 Qy 7 DIAPIUDGSGTIPHDPRMKEFVSTMQLKSKRTFLSMOYSBEPRIHPTKEFQNNP 66
 Db 5 DIAPIUDGSGTIPHDPRMKEFVSTMQLKSKRTFLSMOYSBEPRIHPTKEFQNNP 66
 Db 67 NPSLVKETOTLIGRHTATGIRKVRLBLFNTGARKNPKFLVYTDGEKGDPGLYB 126
 Db 65 DPDALLKHVKHMUINFGAIVNATEPFREELGAPDVKLVLITDE--ATESGNI 122
 Qy 127 DIPEDADEGVIVYVGKQDAPRSERKSERELNTASKPPDADYFQVNNEFALKTONQL 186
 Db 123 DIAKD---IIRYIGKHPQTKESQETLHKPASFVKLDTPEKLDFLTQ 177
 Qy 187 EK 188
 Db 178 KK 179

RESULT 7
 Sequence 7, Application US/09/795798
 Patent No. 6700108
 GENERAL INFORMATION:
 APPLICANT: Preata, Leonard G.
 JARDIE, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/795, 798
 FILING DATE: 28-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974, 899
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELFAX: 650/932-9881
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLogy: Linear
 US-08-974-899-8

Query Match 29.2%; Score 281.5; DB 3; Length 184;
 Best Local Similarity 33.0%; Prod. No. 1.3e-22; Indels 7; Gaps 2;
 Matches 60; Conservative 48; Mismatches 67; Sequence ID: 9;

Qy 7 DIAFLDGGSIIDPFRMKEFVSTMEQLKSKTKLPSLMQYSBFRHTRPFQNP 66
 Db 5 DIAFLDGGSIIDPFRMKEFVSTMEQLKSKTKLPSLMQYSBFRHTRPFQNP 64

Qy 67 NPSILVKPIOTLGRHTATGIRKVVERLFNTINGARKNAFKILVWITDGEKFDPGLYB 126
 Db 65 DPAALLERKHEMLINTFGANTVATEYFREBLGAPDTKVLIIIDGK-ATDSGRI 122

Qy 127 DVPIDEADREGVTVIGVEDAFRSERNSRQLATIASKPDIHYFOVNNEFAKTIONOLR 186
 Db 123 DAAKD----TIRVIGICKHPTQESQETLKASKPASEFVLDLFDKLDFELQ 177

Qy 187 EK 188
 Db 178 KK 179

RESULT 10
 PCT-US96-01314-61

: Sequence 61, Application PC/rus9601314

: GENERAL INFORMATION:
 APPLICANT: M. Brian Arnout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

: COMPUTER READABLE FORM:
 COMPUTER TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PC/2 Model 502 or 555X
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01314
 FILING DATE: 30-JAN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/380,167
 FILING DATE: 30-JAN-95
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Freeman
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-6906
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 amino acids
 TYPE: amino acid
 STRANDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

PCT-US96-01314-61

Query Match 27.6%; Score 266; DB 5; Length 181;
 Best Local Similarity 33.0%; Prod. No. 6e-21; Indels 8; Gaps 3;
 Matches 60; Conservative 46; Mismatches 68; Sequence ID: 8;

Qy 1 CPQDSIAPLIDGGSITPHDRMKSFVSTMEQLKSKTKLPSLMQYSBFRHTRPFK 60
 Db 1 CIKANVLLVPLDGSMELQDDEQKILDFMDYKLNTSYOPAQFTSYKTSDFDS 60

Qy 61 BFOQNNPNSPLYKPTIOLGRHTATGIRKVVERLFNTINGARKNAFKILVWITDGEKPG 120
 Db 61 DYVKWDQDPLAKHYNMMLLTIFGALINYAVATEYFREBLGAPDTKVLIIIDGK-A 118

SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8;

Query Match 29.2%; Score 281.5; DB 4; Length 184;
 Best Local Similarity 33.0%; Prod. No. 1.3e-22; Indels 7; Gaps 2;
 Matches 60; Conservative 48; Mismatches 67; Sequence ID: 9;

Qy 7 DIAFLDGGSIIDPFRMKEFVSTMEQLKSKTKLPSLMQYSBFRHTRPFQNP 66
 Db 5 DIAFLDGGSIIDPFRMKEFVSTMEQLKSKTKLPSLMQYSBFRHTRPFQNP 64

Qy 121 DPLCDEVIPRABRGVIVGVGDAFRSEKSRQELNTIASKPDIHYFOVNNEFAKTIONOLR 179
 Db 119 TDSCNIDAAD-----TIRVIGICKHPTQESQETLKASKPASEFVLDLFDKLDFELQ 173

Qy 180 TI 181

Db 174 DL 175

RESULT 11
 Sequence 50 Application US/08476062A-50
 Patent No. 59125
 GENERAL INFORMATION:
 APPLICANT: Arnaout, M. Anan
 TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESS/B: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08476062A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08216.081
 FILING DATE: 21-MAR-1994
 APPLICATION NUMBER: 07637.830
 FILING DATE: 04-JAN-1991
 APPLICATION NUMBER: 07539.842
 FILING DATE: 16-JUN-1990
 APPLICATION NUMBER: 07412.573
 FILING DATE: 26-JUN-1988
 PRIOR/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/068003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-8070
 TELEX: 617/542-8906

Query Match Score 171; DB 5; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 33; Conservative 0; Indels 0; Gaps 0;

Qy 105 NAFKILVVTIDGKFGDPGLGYEDVTPAAREGV 137
 Db 1 NAFKILVVTIDGKFGDPGLGYEDVTPAAREGV 33

RESULT 13
 US-08-476-062A-10
 Sequence 10 Application US/08476062A
 GENERAL INFORMATION:
 APPLICANT: Arnaout, M. Anan
 TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08476062A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08216.081
 FILING DATE: 21-MAR-1994
 APPLICATION NUMBER: 07637.830
 FILING DATE: 04-JAN-1991
 APPLICATION NUMBER: 07539.842
 FILING DATE: 16-JUN-1990
 APPLICATION NUMBER: 07412.573
 FILING DATE: 26-JUN-1988

RESULT 12
 PCT-US96-01314-50
 Sequence 50 Application PC/US9601314
 GENERAL INFORMATION:
 APPLICANT: M. Anan Arnaout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street

ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/088003
 TELEPHONE: 617/542-5070
 TELFAX: 617/542-8906
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-476-062A-10

Query Match Similarity 15.1%; Score 146; DB 20; Length 28;
 Best Local Similarity 10.0%; Pred. No. 5.1e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 107 FKILVVITDGEKPGDPLGYEDVPIEADR 134
 Db 1 FKILVVITDGEKPGDPLGYEDVPIEADR 28

RESULT 14
 PCT-US96-01314-10

Sequence 10. Application PC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: M. Amin Arnaout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01314
 FILING DATE: 30-JAN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/380,167
 FILING DATE: 30-JAN-95
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Freeman
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONES: (617) 542-5070
 TELFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: amino acid
 STRANDBNESS:
 TOPOLOGY: linear
 PCT-US96-01314-10

Query Match Similarity 15.1%; Score 146; DB 5; Length 28;
 Best Local Similarity 10.0%; Pred. No. 5.1e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 107 FKILVVITDGEKPGDPLGYEDVPIEADR 134

RESULT 15
 US-08-476-062A-8

Sequence 8. Application US/08476062A
 Patent No. 587725
 GENERAL INFORMATION:
 APPLICANT: Arnaout, M. Amin
 TITLE OF INVENTION: CONTROLLING CELULAR IMMUNE/INFLAMMATORY RESPONSES WITH BETA2 INTEGRINS
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSQL for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 07-JUN-1995
 FILING DATE: 07-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/216,081
 FILING DATE: 21-MAR-1994
 APPLICATION NUMBER: 07/637,830
 FILING DATE: 04-JAN-1991
 APPLICATION NUMBER: 07/539,842
 FILING DATE: 18-JUN-1990
 APPLICATION NUMBER: 07/212,573
 FILING DATE: 28-JUN-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/068003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-476-062A-8

Query Match Similarity 13.4%; Score 129; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Indels 0; Gaps 0;

Qy 66 PNPRSLVKEPTOLIGRHTATGIRK 90
 Db 1 PNPRSLVKEPTOLIGRHTATGIRK 25

Search completed: November 14, 2005, 17:39:04
 Job time : 14 secs

Qy 65 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 124
 Db 61 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 120
 Qy 125 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 184
 Db 121 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 2

US-10-346-063-37
 Sequence 37, Application US/10346863
 Publication No. US20040038435A1
 GENERAL INFORMATION:
 APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
 APPLICANT: FAGAN, RICHARD JOSEPH
 APPLICANT: GOTTERIDGE, ALEX
 FILE REFERENCE: 674575-201
 CURRENT APPLICATION NUMBER: US/10/346,863
 CURRENT FILING DATE: 2003-01-17
 PRIOR APPLICATION NUMBER: PCT/GB01/03318
 PRIOR FILING DATE: 2001-07-24
 PRIOR APPLICATION NUMBER: GB 0018126.3
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: GB 0025447.4
 PRIOR FILING DATE: 2000-01-17
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 37
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-346-063-37

Query Match 97.3%; Score 939; DB 15; Length 187;
 Best Local Similarity 100.0%; Pred. No. 7.5e-32;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 DSDIALIDSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFKEFON 64
 Db 1 DSDIALIDSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFKEFON 60
 Qy 65 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 124
 Db 61 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 120
 Qy 125 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 184
 Db 121 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 3

US-10-615-515-9 Application US/10615515
 Sequence 9, Application US/10615515
 Publication No. US20040132974A1
 GENERAL INFORMATION:
 APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
 APPLICANT: FAGAN, RICHARD JOSEPH
 APPLICANT: GOTTERIDGE, ALEX
 FILE REFERENCE: 674575-204
 CURRENT APPLICATION NUMBER: US/10/615,515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107

PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: GB 0100750.9
 PRIOR FILING DATE: 2001-01-11
 NUMBER OF SEQ ID NOS: 12
 SEQ ID NO: 9
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-615-515-9

Query Match 97.3%; Score 939; DB 15; Length 187;
 Best Local Similarity 100.0%; Pred. No. 7.5e-32;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 DSDIALIDSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFKEFON 64
 Db 1 DSDIALIDSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFKEFON 60
 Qy 65 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 124
 Db 61 NNPRLSLVYKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFGDPGL 120
 Qy 125 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 184
 Db 121 YEDVIPADREGVTVIGVDAFRSKERSKQLNTIASPKPRDHVFQVNNEALKTQN 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 4

US-11-000-473-59
 Sequence 59, Application US/11000473
 Publication No. US20040227296A1
 GENERAL INFORMATION:
 APPLICANT: Arndt, M. Armin
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
 FILE REFERENCE: 00786-267002
 CURRENT APPLICATION NUMBER: US/11/000,473
 CURRENT FILING DATE: 2004-11-30
 PRIOR APPLICATION NUMBER: US/09/592,617
 PRIOR FILING DATE: 2000-06-13
 PRIOR APPLICATION NUMBER: US/08/390,167
 PRIOR FILING DATE: 1999-01-30
 PRIOR APPLICATION NUMBER: US/08/216,081
 PRIOR FILING DATE: 1994-03-21
 PRIOR APPLICATION NUMBER: US/07/637,830
 PRIOR FILING DATE: 1991-01-04
 PRIOR APPLICATION NUMBER: US/07/539,842
 PRIOR FILING DATE: 1990-06-18
 PRIOR APPLICATION NUMBER: US/07/212,573
 PRIOR FILING DATE: 1988-06-28
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 59
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-000-473-59

Query Match 55.3%; Score 534; DB 20; Length 187;
 Best Local Similarity 55.6%; Pred. No. 1.5e-48;
 Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;
 Qy 1 CPOEDSIPLIDSGSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFK 60
 Db 1 CPOEDSIPLIDSGSGSII1PHDRMKPYSTMBLKSKTLMSQSEPRHTTFK 60
 Qy 61 EFPQNNPBPRLVKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFG 120
 Db 61 EFPQNNPBPRLVKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFG 120
 Db 61 EFPQNNPBPRLVKPTIOLGLRTTATGIRKVVRBLNITNGARGNAFKLVLVITDGSKFG 120

Qy 121 DPLGDEVIPEDRGVTVYIGDARFSRSKRSQBLNTIASKPRDHIVFVNNEALKT 180
Db 121 BSLDKDVPMDAAGIIRAYGVLAQNRMNSKELNDASKPSQEHIFKDALKD 180
Qy 181 1QNLRE 187
Db 181 1QNLKB 187

RESULT 5
US-09-976-782-38 Application US/03976782
; Sequence 38, Application US/03976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Gross et al.
; TITLE OF INVENTION: No. US20030190715A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976, 782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/244, 113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240, 652
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241, 190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262, 455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240, 648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 38
LENGTH: 176
TYPE: PPT
ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Description of Artificial Sequence : Consensus
OTHER INFORMATION: sequence
US-09-976-782-38

Query Match 34 61 ; Score 331.5; DB 10; Length 176;
Best Local Similarity 43 41; Pred. No. 3.6e-27;
Matches 79; Conservative 29; Mismatches 65; Indels 9; Gaps 4;

Qy 7 DIAFLGSSSIHPFRKKEVSTVMEQLK-KAKTLPSLMOYSEBEFRHTEKFQDN 64
Db 1 DIAFLGSSSIHPFRKKEVSTVMEQLK-PVERLIDPGOKVGLVQSYNRTFLNDYQDN 60

Qy 65 NPNRSPVMPPTQL-LGRTHATGIRKVRLRFNTNGARNKAFLWVITGEKFGDFPL 123
Db 61 KDEVQLAKKIQYCGCTTGALQYVNRNLTPEASGRGAKVWLUTGRSDQPL 120

Qy 124 GDEVIPEDRGVTVYIGDARFSRSKRSQBLNTIASKPRDHIVFVNNEALKT 183
Db 121 --RDVLNELKKGAVNPAIGMADNV---ELRSLSKDEGHVKYSDDEALDILQE 174

Qy 184 OI 185
Db 175 LI 176

US-10-346-863-33 Application US/10346863
; Sequence 33, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADMISSION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346, 863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0019326, 3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447, 4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 33
LENGTH: 182
TYPE: PPT
ORGANISM: Homo sapiens
US-10-346-863-33

Query Match 29.7%; Score 286.5; DB 15; Length 182;
Best Local Similarity 33.5%; Pred. No. 4e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLGSSSIHPFRKKEVSTVMEQLK-LMOYSEBEFRHTEKFQDN 66
Db 4 DIAFLGSSSIHPFRKKEVSTVMEQLK-MDVNLKLNTSPOFANVQFTSYKTFDFSDYVRK 63

Qy 67 NPLSLVKPITQOLQHTATGIRKVRLRFNTNGARNKAFLWVITGEKFGDFPLGYE 126
Db 64 DPDLAKUHYKMLLTNGA NYVATEVFBLSGRDPAKTVLITDQB--APDSNI 121

Qy 127 DVIPEADRGSVIYIGDARFSRSKRSQBLNTIASKPRDHIVFVNNEALKT 186
Db 122 DAAD-----IIRVIGIGHQTKESETLHKFASKPASEFVKLUDTBKQDULFELQ 176

Qy 187 EK 188
Db 177 KK 178

RESULT 7
US-10-346-863-20 Application US/10346863
; Sequence 20, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADMISSION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346, 863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0019326, 3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447, 4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 20
LENGTH: 183
TYPE: PPT
ORGANISM: Homo sapiens
US-10-346-863-20

Query Match 29.7%; Score 286.5; DB 15; Length 183;

Best Local Similarity 33.5%; Pred. No. 4e-22; Mismatches 61; Conservative 47; Indels 67; Gaps 2;

Query 7 DIAFLIDGSSITPDRMKRKEPVSTMQLKSKRTFSIAMSSEBFERHPTKFQPRQNP 66
 Db 4 DIAFLIDGSSITPDRMKRKEPVSTMQLKSKRTFSIAMSSEBFERHPTKFQPRQNP 66
 Qy 67 NPIRSVLRPTOLIGRHTATGKVRBLPNTINGARKNPKILVVTDBKGDPLEY 126
 Db 64 DDAALKHVHMULLNFGAINVATEFREELGARDPDKVLLTDE-ATDSN1 121
 Qy 127 DVIPEADREGVIVYGVGDAFSEKSROEINTASKPRDHFVQVNNEAKTIONQL 186
 Db 122 DAAKD---IIRYIGKHFOTKSSQETLHKFASKPASBFVKLDTFLQ 176
 Qy 187 EK 188
 Db 177 KK 178

RESULT 8
 Sequence 41; Application US/10346863
 Publication No. US20100381375A1
 GENERAL INFORMATION:
 APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
 APPLICANT: PAGAN, RICHARD JOSEPH
 APPLICANT: BUTTERIDGE, ALEX
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-2001
 CURRENT APPLICATION NUMBER: US/10/346,863
 PRIOR APPLICATION NUMBER: PCT/GB01/03318
 PRIOR FILING DATE: 2003-01-17
 PRIOR APPLICATION NUMBER: GB01/03318
 PRIOR FILING DATE: 2001-07-24
 PRIOR APPLICATION NUMBER: GB 0018.126 .3
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: GB 0025447 .4
 NUMBER OF SEQ ID NOS: 57
 SEQ ID NO: 11
 LENGTH: 133
 TYPE: PT
 ORGANISM: Homo sapiens
 US-10-346-663-41

Query Match 29.7%; Score 286.5; DB 15; Length 181;
 Best Local Similarity 33.5%; Pred. No. 4e-22; Mismatches 61; Conservative 47; Indels 67; Gaps 2;

Query 7 DIAFLIDGSSITPDRMKRKEPVSTMQLKSKRTFSIAMSSEBFERHPTKFQPRQNP 66
 Db 4 DIAFLIDGSSITPDRMKRKEPVSTMQLKSKRTFSIAMSSEBFERHPTKFQPRQNP 66
 Qy 67 NPIRSVLRPTOLIGRHTATGKVRBLPNTINGARKNPKILVVTDBKGDPLEY 126
 Db 64 DDAALKHVHMULLNFGAINVATEFREELGARDPDKVLLTDE-ATDSN1 121
 Qy 127 DVIPEADREGVIVYGVGDAFSEKSROEINTASKPRDHFVQVNNEAKTIONQL 186
 Db 122 DAAKD---IIRYIGKHFOTKSSQETLHKFASKPASBFVKLDTFLQ 176
 Qy 187 EK 188
 Db 177 KK 178

RESULT 10
 Sequence 4; Application US/09805356
 Publication No. US20030107875A1
 GENERAL INFORMATION:
 APPLICANT: Li, Rui; Xiong, Jian-Ping
 APPLICANT: Arinou, M.; Main
 FILE REFERENCE: 00716-53601
 CURRENT APPLICATION NUMBER: US/09/805,254
 PRIOR APPLICATION NUMBER: 2002-06-04
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: US/09/805,254
 PRIOR FILING DATE: 2000-07-31
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 184
 TYPE: PT
 ORGANISM: Homo sapiens
 US-09-805-354-4

Query Match 29.7%; Score 286.5; DB 10; Length 184;
 Best Local Similarity 33.0%; Pred. No. 4.e-22; Mismatches 62; Conservative 49; Indels 7; Gaps 2;

Query 1 CPOEDSPNIPALIDSGSGTIPHDRPMKPVSTMEQIKKTSKTSWNOVSFRTHFTFK 60
 Db 1 CIGKAVDVLVLPDESSMSLQDDEKQILDKMKGKLNITSYOFAAVCFTSYKBEFPS 60
 Qy 61 BEQNPNPNSLKP TOLLARHTATGKVRBLLNTMKGKNAKLUVWITDGKFG 120

Db 61 DTVKWKDPDALLKHVKHMLLTNTFGAINYVATEVPRELGARPDATKVLLITDGE-A 118
 Qy 121 DPGYBDVIPADERGIVYIGDAPRSKSROBLNTASKPRDHVFOVNNEALKT 180
 Db 119 TDSGNIDAARD----IRYIIGIGHFOTKESQETLHKPASKPASEVKILDFKLKD 173
 Qy 181 IONQUREK 188
 Db 174 LPTELQCK 181

RESULT 11
 : Sequence 7. Application US/09795798
 : Publication No. US20030267316A1
 : GENERAL INFORMATION:
 : APPLICANT: Preeta, Leonard G.
 : Jardien, Paula M.
 : TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatin (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/795,798
 : FILING DATE: 28-Feb-2001
 : CLASSIFICATION: <Unknown>
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: 08/974,499
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lee, Wendy M.
 : REGISTRATION NUMBER: 40,379
 : REFERENCE/DOCKET NUMBER: P1014R1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650/925-3994
 : FAX: 650/925-3994
 : INFORMATION FOR SEQ ID NO: 7:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 18 amino acids
 : TYPE: Amino Acid
 : TOPOLOGY: Linear
 : SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 us-09-795-798-7

Query Match Score 29.7%; Best Local Similarity 33.5%; Pred. No. 4.1e-22; Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Db 7 DIAFDGGSITPHIDPRMKKEVTEHQIKSKTLPSLWQSEEFRIHTPEFQNNP 66
 5 DLFLPGGMSIQPEFOKIDMKDVKKLNTSQPAQQTSTKTFPSDYTKRK 64
 67 NPSLYKPTIOLGRHTATGIRKVRELPLNTGARKNAKPKLUVVTDGEKFDPGLYS 126
 65 DDALAKHVKHMLLTNTFGAINYVATEVPRELGARPDATKVLLITDGB-AADSGNI 122
 127 DVIPEADREGIVYIGDAPRSKSROBLNTASKPRDHVFOVNNEALKTQQLR 186
 123 DAaKQ----IRYIIGIGHFOTKESQETLHKPASKPASEVKILDFKLKDPELQ 177
 187 EK 188
 178 KK 179

RESULT 12
 : Sequence 4. Application US/09758493
 : Publication No. US20030086635A1
 : GENERAL INFORMATION:
 : APPLICANT: Arnaut, M. Amain
 : APPLICANT: Xiong, Jian-Ping
 : TITLE OF INVENTION: HIGH EFFICIENCY INTEGRIN POLYPEPTIDES AND
 : PEPTIDE RESPECTIVE: 098604001
 : CURRENT APPLICATION NUMBER: US/09/758,493
 : CURRENT FILING DATE: 2001-01-11
 : PRIOR APPLICATION NUMBER: US 60/221,950
 : PRIOR FILING DATE: 2000-07-31
 : NUMBER OF SEQ ID NOS: 20
 : SOFTWARE: FastSEQ for Windows Version 4.0
 : SEQ ID NO: 4 LENGTH: 184
 : TYPE: PRIM
 : ORGANISM: Homo sapiens
 : US-09-758-493-4

Query Match Score 29.7%; Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;

Db 1 CPQDSDIALDGSITPHIDPRMKKEVTEHQIKSKTLPSLWQSEEFRIHTPEF 60
 1 CIRKNVNDLPFLDPSMSLQDEFQNLDFKDNMKLNNTSYOFAVQPTSYKTSFPPS 60
 61 EFQNNPENPRLVXPVTPOLGRHTATGIRKVRELPLNTGARKNAKPKLUVVTDGEKF 120
 61 DYVKKWDPDALAKHVKHMLLTNTFGAINYVATEVPRELGARPDATKVLLITDGE-A 118
 Qy 121 DPGYBDVIPADERGIVYIGDAPRSKSROBLNTASKPRDHVFOVNNEALKT 180
 Db 119 TDGNTDAKD---IRYIIGIGHFOTKESQETLHKPASKPASEVKILDFKLKD 173
 Qy 181 IONQUREK 188
 Db 174 LPTELQCK 181

RESULT 13
 : Sequence 4. Application US/10144259
 : Publication No. US20031010691A1
 : GENERAL INFORMATION:
 : APPLICANT: Arnaut, M. Amain
 : APPLICANT: Xiong, Jian-Ping
 : TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
 : FILE REFERENCE: 0078654001
 : CURRENT APPLICATION NUMBER: US/10/144,259
 : CURRENT FILING DATE: 2002-09-04
 : PRIOR APPLICATION NUMBER: US 09/758,493
 : PRIOR FILING DATE: 2001-01-11
 : PRIOR APPLICATION NUMBER: US 60/221,950
 : PRIOR FILING DATE: 2000-07-31
 : NUMBER OF SEQ ID NOS: 30
 : SOFTWARE: FastSEQ for Windows Version 4.0
 : SEQ ID NO: 4 LENGTH: 184
 : TYPE: PRIM
 : ORGANISM: Homo sapiens
 : US-10-144-259-4

Query Match Score 29.7%; Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;

RESULT 15
US-10-727-737-7
; Sequence 7, Application US/10727737
; Publication No. US20040146507A1

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